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<110> BASF Plant Science GmbH

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<140> PF0000054331

10 <141> 2003-03-07

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<170> PatentIn Ver. 2.1

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11

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20	tac aag aaa caa acc aac ttc gac aac aga ttc aag ctt agt cta aac Tyr Lys Lys Gln Thr Asn Phe Asp Asn Arg Phe Lys Leu Ser Leu Asn	130	135	140	432
25	aag ctc tac gct tgg tct ctc tct gat tat gac cgt gtt gta atg ctt Lys Leu Tyr Ala Trp Ser Leu Ser Asp Tyr Asp Arg Val Val Met Leu	145	150	155	480
30	gat gtc gac aat ctc ttt ctc aag aac acc gac gag ctc ttc cag tgt Asp Val Asp Asn Leu Phe Leu Lys Asn Thr Asp Glu Leu Phe Gln Cys	165	170	175	528
35	ggc caa ttt tgt gct gtc ttc atc aac cct tgc atc ttc cac act ggt Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe His Thr Gly	180	185	190	576
40	ctc ttt gtg ttg cag cca tca atg gag gtc ttt aga gac atg ctt cat Leu Phe Val Leu Gln Pro Ser Met Glu Val Phe Arg Asp Met Leu His	195	200	205	624
45	gag ctt gaa gta aag aga gat aac cct gat gga gct gat caa ggc ttt Glu Leu Glu Val Lys Arg Asp Asn Pro Asp Gly Ala Asp Gln Gly Phe	210	215	220	672
50	ctt gtc agc tac ttc tct gat tta ctc aat cag cct ctc ttt cgt cct Leu Val Ser Tyr Phe Ser Asp Leu Leu Asn Gln Pro Leu Phe Arg Pro	225	230	235	720
55	cct ccc gat aac cgc acc gcg ctt aag gga cat ttt agg ctt cct ttg Pro Pro Asp Asn Arg Thr Ala Leu Lys Gly His Phe Arg Leu Pro Leu	245	250	255	768
60	gga tat caa atg gac gca tct tat tac tac ctt aag ctc aga tgg aac Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu Arg Trp Asn	260	265	270	816
65	gta cca tgt gga cca aac agt gtg ata acg ttc cca gga gca gta tgg Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala Val Trp	275	280	285	864
70	tta aag cca tgg tat tgg tgg tca tgg cct gtt ctt cct tta ggc ctt Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu Gly Leu	290	295	300	912
75	tca tgg cac cac caa cgc cgc tac acg att agt tat tca gca gag atg Ser Trp His His Gln Arg Arg Tyr Thr Ile Ser Tyr Ser Ala Glu Met	305	310	315	960
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	Pro Trp Val Leu Thr Gln Ala Val Phe Tyr Leu Gly Ile Ile Leu Val	
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	Thr Arg Leu Ala Arg Pro Asn Met Thr Lys Leu Cys Tyr Arg Arg Ser	
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	Asp Lys Asn Leu Ser Met Ile Gln Thr Ala Phe Lys Phe Val Ala Leu	
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	Leu Phe Ile Leu Ser Ala Tyr Ile Ile Pro Phe Phe Ile Ile Pro Gln	
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	Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Thr Gly Ser Phe	
25	385 390 395 400	
	gct ctc tct acc ata ccc atc aac gcc ttc ttg ctt ccc att ctc cct	1248
	Ala Leu Ser Thr Ile Pro Ile Asn Ala Phe Leu Leu Pro Ile Leu Pro	
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	Val Ile Thr Pro Trp Leu Gly Ile Phe Gly Thr Leu Leu Val Met Ala	
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	Phe Pro Ser Tyr Pro Asp Gly Val Val Arg Ala Leu Ser Val Phe Gly	
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	Tyr Ala Phe Cys Cys Ala Pro Phe Leu Trp Val Ser Phe Val Lys Ile	
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	Thr Ser His Leu Gln Ile Met Ile Asp Lys Glu Val Leu Phe Pro Arg	
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	Leu Glu Thr Glu Asn Ala Asn Ala Met Thr Ala Val Met Glu Arg Gly	
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	Leu Lys Thr Gln Arg Arg Pro Glu His Lys Asn Ala Tyr Ala Thr Met	
	50 55 60	
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13

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	Glu Glu Asp Gly Ala Lys Val Val Arg Val Glu Asn Leu Glu Asn Pro	115	120	125
	Tyr Lys Lys Gln Thr Asn Phe Asp Asn Arg Phe Lys Ser Leu Asn	130	135	140
10	Lys Leu Tyr Ala Trp Ser Leu Ser Asp Tyr Asp Arg Val Val Met Leu	145	150	155
	Asp Val Asp Asn Leu Phe Leu Lys Asn Thr Asp Glu Leu Phe Gln Cys	165	170	175
15	Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe His Thr Gly	180	185	190
	Leu Phe Val Leu Gln Pro Ser Met Glu Val Phe Arg Asp Met Leu His	195	200	205
	Glu Leu Glu Val Lys Arg Asp Asn Pro Asp Gly Ala Asp Gln Gly Phe	210	215	220
20	Leu Val Ser Tyr Phe Ser Asp Leu Leu Asn Gln Pro Leu Phe Arg Pro	225	230	235
	Pro Pro Asp Asn Arg Thr Ala Leu Lys Gly His Phe Arg Leu Pro Leu	245	250	255
25	Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu Arg Trp Asn	260	265	270
	Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala Val Trp	275	280	285
	Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu Gly Leu	290	295	300
30	Ser Trp His His Gln Arg Tyr Thr Ile Ser Tyr Ser Ala Glu Met	305	310	315
	Pro Trp Val Leu Thr Gln Ala Val Phe Tyr Leu Gly Ile Ile Leu Val	325	330	335
35	Thr Arg Leu Ala Arg Pro Asn Met Thr Lys Leu Cys Tyr Arg Arg Ser	340	345	350
	Asp Lys Asn Leu Ser Met Ile Gln Thr Ala Phe Lys Phe Val Ala Leu	355	360	365
	Leu Phe Ile Leu Ser Ala Tyr Ile Ile Pro Phe Phe Ile Ile Pro Gln	370	375	380
40	Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Thr Gly Ser Phe	385	390	395
	Ala Leu Ser Thr Ile Pro Ile Asn Ala Phe Leu Leu Pro Ile Leu Pro	405	410	415
45	Val Ile Thr Pro Trp Leu Gly Ile Phe Gly Thr Leu Leu Val Met Ala	420	425	430
	Phe Pro Ser Tyr Pro Asp Gly Val Val Arg Ala Leu Ser Val Phe Gly	435	440	445
	Tyr Ala Phe Cys Cys Ala Pro Phe Leu Trp Val Ser Phe Val Lys Ile	450	455	460
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	Gln	Pro	Pro	Gln	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Asn	Ala	Val	Val	Thr	
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	Val	Gln	Asp	Arg	Gly	Leu	Lys	Thr	Arg	Arg	Pro	Glu	His	Lys	Asn	Ala	
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	Tyr	Ala	Thr	Met	Met	Tyr	Met	Gly	Thr	Pro	Arg	Asp	Tyr	Glu	Phe	Tyr	
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	Val	Ala	Thr	Arg	Val	Leu	Ile	Arg	Ser	Leu	Arg	Ser	Leu	His	Val	Glu	
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30	gct	gat	ctc	gtc	gtc	atc	gct	tct	ctc	gac	gtt	cct	ctc	cga	tgg	gtt	336
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	Gln	Thr	Leu	Glu	Glu	Glu	Asp	Gly	Ala	Lys	Val	Val	Arg	Val	Glu	Asn	
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	Val	Val	Met	Leu	Asp	Ala	Asp	Asn	Leu	Phe	Leu	Lys	Lys	Ala	Asp	Glu	
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	Leu	Phe	Gln	Cys	Gly	Arg	Phe	Cys	Ala	Val	Phe	Ile	Asn	Pro	Cys	Ile	
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	Phe	His	Thr	Gly	Leu	Phe	Val	Leu	Gln	Pro	Ser	Val	Glu	Val	Phe	Lys	
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15

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	Arg Arg Ser Asp Arg Asn Leu Thr Thr Ile Gln Ala Gly Phe Lys Leu	
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	Ile Ala Leu Leu Ser Val Val Ala Ala Tyr Ile Phe Pro Phe Phe Thr	
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	Thr Leu Pro Val Leu Thr Pro Trp Leu Gly Ile Leu Gly Thr Leu Leu	
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55	gtc atg gcc ttc cct tgg tac cct gat gga gtg gtc aga gcc ttg tca	1344
	Val Met Ala Phe Pro Trp Tyr Pro Asp Gly Val Val Arg Ala Leu Ser	
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	Val Phe Ala Tyr Ala Phe Cys Cys Ala Pro Phe Val Trp Val Ser Phe	
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16

Arg Lys Ile Thr Ser His Leu Gln Val Leu Ile Glu Lys Glu Val Leu
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 Gln Thr Leu Glu Glu Glu Asp Gly Ala Lys Val Val Arg Val Glu Asn
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17

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 Ser Ser Gln Ser Ser His Arg Leu Tyr Ile Ser Ser Glu Lys Thr Lys
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 Thr Lys Arg Phe Gln Arg Asn Gly Tyr Thr Leu Asp Val Glu Met Cys
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 Val Asn Phe Ser Ser Leu Lys Leu Val Leu Phe Leu Met Met Leu Val
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 85 90 95
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18

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	Pro	Asp	Lys	Ser	Arg	Ile	Asp	Leu	Ile	Ile	Ala	Lys	Leu	Pro	Cys	Asn	
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21

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23

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			355					360					365				
75	gcg	ttt	ggg	gta	agg	ttt	gat	gat	cgt	gtc	acg	ggt	aaa	ctt	gag	gct	1152
	Ala	Phe	Gly	Val	Arg	Phe	Asp	Asp	Arg	Val	Thr	Gly	Lys	Leu	Glu	Ala	

	370	375	380	
5	ttt gct agt agg gct aag att gtt cat att gat att gac tcg gct gag Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu 385 390 395 400	1200		
10	att ggg aag aat aag act cct cat gtg tct gtg tgt ggt gat gtt aag Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys 405 410 415	1248		
15	ctg gct ttg caa ggg atg aat aag gtt ctt gag aac cga gcg gag gag Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu 420 425 430	1296		
20	ctt aaa ctt gat ttt gga gtt tgg agg aat gag ttg aac gta cag aaa Leu Lys Leu Asp Phe Gly Val Trp Arg Asn Glu Leu Asn Val Gln Lys 435 440 445	1344		
25	cag aag ttt ccg ttg agc ttt aag acg ttt ggg gaa gct att cct cca Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro 450 455 460	1392		
30	cag tat gcg att aag gtc ctt gat gag ttg act gat gga aaa gcc ata Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu Thr Asp Gly Lys Ala Ile 465 470 475 480	1440		
35	ata agt act ggt gtc ggg caa cat caa atg tgg gcg gcg cag ttc tac Ile Ser Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr 485 490 495	1488		
40	aat tac aag aaa cca agg cag tgg cta tca tca gga ggc ctt gga gct Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser Ser Gly Gly Leu Gly Ala 500 505 510	1536		
45	atg gga ttt gga ctt cct gct gcg att gga gcg tct gtt gct aac cct Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro 515 520 525	1584		
50	gat gcg ata gtt gtg gat att gac gga gat gga agt ttt ata atg aat Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn 530 535 540	1632		
55	gtg caa gag cta gcc act att cgt gta gag aat ctt cca gtg aag gta Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Val 545 550 555 560	1680		
60	ctt tta tta aac aac cag cat ctt ggc atg gtt atg caa tgg gaa gat Leu Leu Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu Asp 565 570 575	1728		
65	cgg ttc tac aaa gct aac cga gca cac aca ttt ctc gga gat ccg gct Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Phe Leu Gly Asp Pro Ala 580 585 590	1776		
70	cag gag gac gag ata ttc ccg aac atg ttg ctg ttt gca gca gct tgc Gln Glu Asp Glu Ile Phe Pro Asn Met Leu Leu Phe Ala Ala Ala Cys 595 600 605	1824		
75	ggg att cca gcg gcg agg gtg aca aag aaa gca gat ctc cga gaa gct Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Ala Asp Leu Arg Glu Ala 610 615 620	1872		

att cag aca atg ctg gat aca cca gga cct tac ctg ttg gat gtg att 1920
 Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile
 625 630 635 640
 5 tgt ccg cac caa gaa cat gtg ttg ccg atg atc ccg aat ggt ggc act 1968
 Cys Pro His Gln Glu His Val Leu Pro Met Ile Pro Asn Gly Gly Thr
 645 650 655
 10 ttc aac gat gtc ata acg gaa gga gat ggc cgg att aaa tac tgagagctc 2019
 Phe Asn Asp Val Ile Thr Glu Gly Asp Gly Arg Ile Lys Tyr
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 25 Ser Thr Lys Pro Ser Pro Ser Ser Ser Lys Ser Pro Leu Pro Ile Ser
 20 25 30
 Arg Phe Ser Leu Pro Phe Ser Leu Asn Pro Asn Lys Ser Ser Ser Ser
 35 40 45
 30 Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser Pro Ser Ser Ile Ser Ala
 50 55 60
 35 Val Leu Asn Thr Thr Thr Asn Val Thr Thr Thr Pro Ser Pro Thr Lys
 65 70 75 80
 Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg Phe Ala Pro Asp Gln Pro
 85 90 95
 40 Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly Val
 100 105 110
 Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu Ile His Gln
 115 120 125
 45 Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn Val Leu Pro Arg His Glu
 130 135 140
 50 Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly Lys
 145 150 155 160
 Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 165 170 175
 55 Ser Gly Leu Ala Asp Ala Leu Leu Asp Ser Val Pro Leu Val Ala Ile
 180 185 190
 Thr Gly Gln Val Pro Arg Arg Met Ile Gly Thr Asp Ala Phe Gln Glu
 195 200 205
 60 Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His Asn Tyr Leu
 210 215 220

Val Met Asp Val Glu Asp Ile Pro Arg Ile Ile Glu Glu Ala Phe Phe
 225 230 235 240
 5 Leu Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro Lys
 245 250 255
 Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn Trp Glu Gln Ala Met Arg
 260 265 270
 10 Leu Pro Gly Tyr Met Ser Arg Met Pro Lys Pro Pro Glu Asp Ser His
 275 280 285
 Leu Glu Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Lys Pro Val Leu
 290 295 300
 Tyr Val Gly Gly Gly Cys Leu Asn Ser Ser Asp Glu Leu Gly Arg Phe
 305 310 315 320
 20 Val Glu Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly
 325 330 335
 Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu His Met Leu Gly Met His
 340 345 350
 25 Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu
 355 360 365
 Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala
 370 375 380
 Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu
 385 390 395 400
 35 Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys
 405 410 415
 Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu
 420 425 430
 40 Leu Lys Leu Asp Phe Gly Val Trp Arg Asn Glu Leu Asn Val Gln Lys
 435 440 445
 Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro
 450 455 460
 Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu Thr Asp Gly Lys Ala Ile
 465 470 475 480
 50 Ile Ser Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr
 485 490 495
 Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser Ser Gly Gly Leu Gly Ala
 500 505 510
 55 Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro
 515 520 525
 Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn
 530 535 540
 60

41

Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Val
 545 550 555 560

5 Leu Leu Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu Asp
 565 570 575

Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Phe Leu Gly Asp Pro Ala
 580 585 590

10 Gln Glu Asp Glu Ile Phe Pro Asn Met Leu Leu Phe Ala Ala Ala Cys
 595 600 605

Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Ala Asp Leu Arg Glu Ala
 610 615 620

15 Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile
 625 630 635 640

20 Cys Pro His Gln Glu His Val Leu Pro Met Ile Pro Asn Gly Gly Thr
 645 650 655

Phe Asn Asp Val Ile Thr Glu Gly Asp Gly Arg Ile Lys Tyr
 660 665 670

25

<210> 18
 <211> 259
 <212> DNA
 30 <213> Artificial Sequence

<220>
 <221> promoter
 <222> (1)..(259)

35

<220>
 <223> Description of Artificial Sequence:be2promoter
 fragment

40 <400> 18
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 acataagtca ttttaactga agctgcattg atgaaaaatt atactatgtc tttatgtata 120
 tatattaatg ttttaaatc ctttatagtg ataaagatgg ttcgaaacat gctacaaatt 180
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 45 tagataccag cccgggccc 259

<210> 19
 <211> 400
 50 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RNAi420be2be1

55 <220>

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 ggatgtggga ttcccgcctc ttttaactatg gaaactggga ggtacttagg tatcttctct 180

42

caaatgcgag atggttggtt ccatttcaca tcaccagaag gaatacctgg agttccagaa 240
 acaaatttca atggtcgtcc aaattccttc aaagtgtgtg ctctgctgcg aacatgtgtg 300
 gcttattaca gagttgacga acgcatgtca gaaactgaag tttaccagac agacatttct 360
 agtgagctac taccaacagc caatatcgag gagagtgcg 400

5

<210> 20

<211> 1105

<212> DNA

10 <213> Artificial Sequence

<220>

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15 <220>

<400> 20

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 ggatgtggga ttcccgctc tttaactatg gaaactggga ggtacttagg tatcttctct 180
 caaatgcgag atggttggtt ccatttcaca tcaccagaag gaatacctgg agttccagaa 240
 acaaatttca atggtcgtcc aaattccttc aaagtgtgtg ctctgctgcg aacatgtgtg 300
 gcttattaca gagttgacga acgcatgtca gaaactgaag tttaccagac agacatttct 360
 agtgagctac taccaacagc caatatcgag gagagtgcg atcaagctga tctctaaata 420
 attcgaaata tctttgttat tatttttttc tattcaaatt gcaattagac ataagtcatt 480
 ttaactgaag ttgcattgat gaaaaattat actatgtttt atgtatatat attaattttt 540
 aaattccttt atagtataaa agatagttcg aaacatgcta taaattatta tacgaattta 600
 cgttactttt tttaatctac tttaacaatt ttctaatttc actattgaac atagatacca 660
 gcccgggccg tcgacctcga attcgccctt ggagagtgcg gttcgcgtca ctctcctcga 720
 tattggctgt tggtagtagc tctactagaa tgtctgtctg gtaaaacttca gtttctgaca 780
 tgcgttcgtc aactctgtaa taagccacac atgttcgcgc aggagacagc actttgaagg 840
 aatttgagc accattgaaa tttgtttctg gaactccagg tattccttct ggtgatgtga 900
 aatggcaacc accatctcgc atttgagaga agatacctaa gtacctccca gtttccatag 960
 ttaaagaggg gggaatccca catccaatga taaccacgag ctccagagtg aaagtaacaa 1020
 ctatcggtgc cgtcaaacat gttcagtcga tctaaagtat tatttgatgc atggctgtga 1080
 acgatgtcca tgagaacaac aattc 1105

40 <210> 21

<211> 180

<212> DNA

<213> Artificial Sequence

<220>

45 <223> Description of Artificial Sequence:SBE RNAi 1

<220>

<400> 21

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 aacagccaat atcgaggaga gtgacgttcg cgtcactctc ctcgatattg gctgttggtg 120
 gtagctcact caaccacat ctgcatttg agagaagata cctaagtacc ttttgggtacc 180

55 <210> 22

<211> 420

<212> DNA

<213> Artificial Sequence

60 <220>

<223> Description of Artificial Sequence:SBE RNAi 2

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 5 ctgggaggta cttagggtatc ttctctcaaa tgcgagatgg tggttggctt attacagagt 120
 tgacgaacgc atgtcagaaa ctgaagttta ccagacagac atttctagtg agctactacc 180
 aacagccaat atcgaggaga gtgacgttcg cgctactctc ctcgatattg gctgttggtg 240
 gtagctcact agaaatgtct gtctggtaaa cttcagtttc tgacatgcgt tcgtcaactc 300
 tgtaataagc caaccacat ctgcatttg agagaagata cctaagtacc tcccagtttc 360
 10 catagttaaa gaggcgggaa tcccacatcc aatgataacc acgagctcca ttttgggtacc 420

<210> 23
 <211> 37
 <212> DNA
 15 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:spacer

20 <220>

<400> 23
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25 <210> 24
 <211> 837
 <212> DNA
 30 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fragment of be2
 and bel in PHAS3 for RNAi

35 <220>

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 ggatgtggga ttccgcctc ttaactatg gaaactggga ggtacttagg tatcttctct 180
 caaatgcgag atggtggttg ccatttcaca tcaccagaag gaatacctgg agttccagaa 240
 acaaatttca atggtcgtcc aaattccttc aaagtgtgt ctctgcgcg aacatgtgtg 300
 gcttattaca gagttgacga acgcatgtca gaaactgaag tttaccagac agacatttct 360
 45 agtgagctac taccaacagc caatatcgag gagagtgcg atcaagctta tcgataccgt 420
 cgacctcgaa gcttgatcgt cactctctc gatattggct gttggtagta gctcactaga 480
 aatgtctgtc tggtaaactt cagtttctga catgcgttcg tcaactctgt aataagccac 540
 acatgttcgc gcaggagaca gcactttgaa ggaatttgga cgaccattga aatttgtttc 600
 tggaactcca ggtattcctt ctggtgatgt gaaatggcaa ccaccatctc gcatttgaga 660
 50 gaagatacct aagtacctc cagtttccat agttaagag gcgggaatcc cacatccaat 720
 gataaccacg agtccagag tgaaagtaac aactatcggt gccgtcaaac atgttcagtc 780
 catctaaagt attatttgat gcatggctgt gaacgatgtc catgagaaca acaattc 837